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Draft Genome Sequence of *Mycobacterium elephantis* Strain Lipa

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We report the draft genome sequence of *Mycobacterium elephantis* strain Lipa from a sputum sample of a patient with pulmonary disease. This is the first draft genome sequence of *M. elephantis*, a rapidly growing mycobacterium.

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Mycobacterium elephantis is a rapidly growing mycobacterium, originally isolated from a lung abscess in an elephant in 2000, that has been occasionally isolated from human clinical samples, most commonly sputum specimens (1–3). *M. elephantis* has also been reported to have been isolated from a cervical lymph node, although its relation to clinical disease is unclear (2). The notable phenotypic characteristics of *M. elephantis* include a relatively slow growth rate for a rapid growing mycobacterium, smooth colonies producing a pale yellow pigment with age, and ability to grow on 5% NaCl in Lowenstein-Jensen medium, along with a unique high-performance liquid chromatography (HPLC) mycolic acid profile (3).

Rapidly growing mycobacteria constitute a commonly isolated population of acid-fast bacillus in the clinical microbiology lab of varying clinical importance (4, 5). We sequenced the first draft genome of *M. elephantis* from a sputum sample of a patient in 2003 with pulmonary disease. The isolate was originally typed as *M. elephantis* based on partial 16S sequencing.

DNA from *M. elephantis* strain Lipa was extracted using the Qiagen EZ1 kit, and paired-end libraries were prepared using the Nextera XT DNA library kit followed by sequencing on an Illumina MiSeq instrument. Sequences were adapter and quality (Q20) trimmed using Cutadapt, *de novo* assembled using SPAdes v3.5, metagenomically screened for contaminating sequence with SURPI, and annotated via Prokka v1.1 (6–9). A total of 9,000,614 paired-end reads of average length 115 nucleotides were recovered after trimming. *De novo* assembly yielded 234 contigs for a total assembly size of 5,187,616 bp with an N_{50} of 42,430 bp, an average coverage of 196×, and a total of 5,022 coding sequences. Contiguity was most likely disrupted by the high G+C content (68%) along with several high-copy-number integrases, transposases, and recombinases that were longer than sequence read length. Other high-copy-number contigs included those containing genes to *mlaE* phospholipid ABC transporter permease, for which *M. elephantis* strain Lipa had 19 different homologs in the genome.

The five closest BLASTN hits to the complete 16S sequence from the isolate were other *M. elephantis* 16S sequences with 99.4 to 100% identity. The Lipa strain contained three putative beta-glucosidase genes. By Comprehensive Antibiotic Resistance Database analysis, the Lipa strain includes an *arr1* rifampin ADP-ribosyl transferase (85% by amino acid to *M. vanbaalenii* PYR-1) and a *blaF* beta-lactamase (10).

Nucleotide sequence accession numbers. This whole-genome shotgun project has been deposited at DDBJ/ENA/GenBank under the accession no. LBNO00000000. The assembly described in this paper is the first version, LBNO01000000.

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